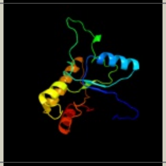
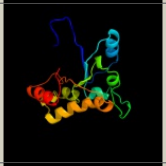
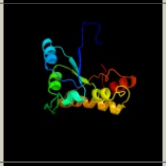
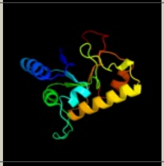
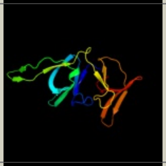
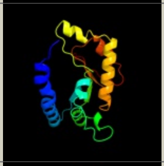
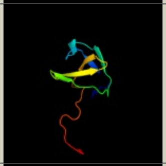
Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P31666
Date	Thu Jan 5 11:48:29 GMT 2012
Unique Job ID	eda3e1311e20fe7b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2j13a1	Alignment		99.9	20	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**NodB-like polysaccharide deacetylase
2	d2iw0a1	Alignment		99.9	21	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**NodB-like polysaccharide deacetylase
3	d2cc0a1	Alignment		99.9	22	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**NodB-like polysaccharide deacetylase
4	c1w17A_	Alignment		99.9	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable polysaccharide deacetylase pdaa; **PDBTitle:** structure of bacillus subtilis pdaa, a family 42 carbohydrate esterase.
5	c2iw0A_	Alignment		99.9	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chitin deacetylase; **PDBTitle:** structure of the chitin deacetylase from the fungal2 pathogen colletotrichum lindemuthianum
6	c2c1iA_	Alignment		99.9	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidoglycan glcnac deacetylase; **PDBTitle:** structure of streptococcus pnemoniae peptidoglycan2 deacetylase (sppgda) d 275 n mutant.
7	d1ny1a_	Alignment		99.9	21	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**NodB-like polysaccharide deacetylase
8	c2w3zA_	Alignment		99.9	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative deacetylase; **PDBTitle:** structure of a streptococcus mutans ce4 esterase
9	c2vyoA_	Alignment		99.9	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chitooligosaccharide deacetylase; **PDBTitle:** chitin deacetylase family member from encephalitozoon2 cuniculi
10	d2c1ia1	Alignment		99.8	20	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**NodB-like polysaccharide deacetylase
11	d2c71a1	Alignment		99.8	18	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**NodB-like polysaccharide deacetylase

12	c3rxzA_	Alignment		99.7	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**polysaccharide deacetylase; **PDBTitle:** crystal structure of putative polysaccharide deacetylase from2 mycobacterium smegmatis
13	c3npfB_	Alignment		99.6	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative dipeptidyl-peptidase vi; **PDBTitle:** crystal structure of a putative dipeptidyl-peptidase vi (bacova_00612)2 from bacteroides ovatus at 1.72 a resolution
14	c3qbuD_	Alignment		99.6	20	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of putative peptidoglyacn deactelyase (hp0310) from2 helicobacter pylori
15	c1xovA_	Alignment		99.6	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ply protein; **PDBTitle:** the crystal structure of the listeria monocytogenes bacteriophage psa2 endolysin plypsa
16	d1z7aa1	Alignment		99.5	14	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**PA1517-like
17	c3s6oD_	Alignment		99.5	13	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**polysaccharide deacetylase family protein; **PDBTitle:** crystal structure of a polysaccharide deacetylase family protein from2 burkholderia pseudomallei
18	d2nlya1	Alignment		99.4	10	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**Divergent polysaccharide deacetylase
19	c2krsA_	Alignment		99.2	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**probable enterotoxin; **PDBTitle:** solution nmr structure of sh3 domain from cpf_0587 (fragment2 415-479) from clostridium perfringens. northeast structural3 genomics consortium (nesg) target cpr74a.
20	c2kt8A_	Alignment		99.2	8	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**probable surface protein; **PDBTitle:** solution nmr structure of the cpe1231(468-535) protein from2 clostridium perfringens, northeast structural genomics3 consortium target cpr82b
21	c3h41A_	Alignment	not modelled	99.1	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nlp/p60 family protein; **PDBTitle:** crystal structure of a nlpc/p60 family protein (bce_2878) from2 bacillus cereus atcc 10987 at 1.79 a resolution
22	c2kq8A_	Alignment	not modelled	99.1	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cell wall hydrolase; **PDBTitle:** solution nmr structure of a domain from bt9727_4915 from2 bacillus thuringiensis, northeast structural genomics3 consortium target bur95a
23	c2kybA_	Alignment	not modelled	99.0	17	**PDB header:**toxin **Chain:** A: **PDB Molecule:**mannosyl-glycoprotein endo-beta-n-acetylglucosamidase **PDBTitle:** solution structure of cpr82g from clostridium perfringens. north east2 structural genomics consortium target cpr82g
24	c1ng2A_	Alignment	not modelled	99.0	18	**PDB header:**oxidoreductase activator **Chain:** A: **PDB Molecule:**neutrophil cytosolic factor 1; **PDBTitle:** structure of autoinhibited p47phox
25	c1m9sA_	Alignment	not modelled	98.8	21	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**internalin b; **PDBTitle:** crystal structure of internalin b (inlb), a listeria2 monocytogenes virulence protein containing sh3-like3 domains.
26	c1ov3A_	Alignment	not modelled	98.7	18	**PDB header:**oxidoreductase activator **Chain:** A: **PDB Molecule:**neutrophil cytosol factor 1; **PDBTitle:** structure of the p22phox-p47phox complex
27	c1griA_	Alignment	not modelled	98.4	18	**PDB header:**signal transduction adaptor **Chain:** A: **PDB Molecule:**growth factor bound protein 2; **PDBTitle:** grb2
28	c2eyzA_	Alignment	not modelled	98.1	11	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**v-crk sarcoma virus ct10 oncogene

28	c2eyzA_	Alignment	not modelled	98.1	11	homolog **PDBTitle:** ct10-regulated kinase isoform ii
29	d1k1xa3	Alignment	not modelled	98.0	13	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**4-alpha-glucanotransferase, N-terminal domain
30	c2l3sA_	Alignment	not modelled	97.7	13	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**autoinhibited crk protein; **PDBTitle:** structure of the autoinhibited crk
31	c3m1uB_	Alignment		97.7	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative gamma-d-glutamyl-l-diamino acid endopeptidase; **PDBTitle:** crystal structure of a putative gamma-d-glutamyl-l-diamino acid2 endopeptidase (dvu_0896) from desulfovibrio vulgaris hildenborough at3 1.75 a resolution
32	c1k1yA_	Alignment	not modelled	97.4	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**4-alpha-glucanotransferase; **PDBTitle:** crystal structure of thermococcus litoralis 4-alpha-glucanotransferase2 complexed with acarbose
33	d2b5dx2	Alignment	not modelled	96.5	5	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**AmyC N-terminal domain-like
34	c2ed0A_	Alignment	not modelled	96.4	20	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**abl interactor 2; **PDBTitle:** solution structure of the sh3 domain of abl interactor 22 (abelson interactor 2)
35	c2pqhA_	Alignment	not modelled	96.3	11	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**spectrin alpha chain, brain; **PDBTitle:** structure of sh3 chimera with a type ii ligand linked to the chain c-2 terminal
36	c2yuoA_	Alignment	not modelled	96.2	13	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**run and tbc1 domain containing 3; **PDBTitle:** solution structure of the sh3 domain of mouse run and tbc12 domain containing 3
37	c2dbmA_	Alignment	not modelled	96.1	16	**PDB header:**transferase, signaling protein **Chain:** A: **PDB Molecule:**sh3-containing grb2-like protein 2; **PDBTitle:** solution structures of the sh3 domain of human sh3-2 containing grb2-like protein 2
38	c2eyyA_	Alignment	not modelled	96.1	14	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**v-crk sarcoma virus ct10 oncogene homolog **PDBTitle:** ct10-regulated kinase isoform i
39	c2ekhA_	Alignment	not modelled	96.1	17	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**sh3 and px domain-containing protein 2a; **PDBTitle:** solution structures of the sh3 domain of human kiaa0418
40	c2dmoA_	Alignment	not modelled	96.0	20	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**neutrophil cytosol factor 2; **PDBTitle:** refined solution structure of the 1st sh3 domain from human2 neutrophil cytosol factor 2 (ncf-2)
41	c2nwmA_	Alignment	not modelled	96.0	8	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**vinexin; **PDBTitle:** solution structure of the first sh3 domain of human vinexin2 and its interaction with the peptides from vinculin
42	c2b5dX_	Alignment	not modelled	95.9	6	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**alpha-amylase; **PDBTitle:** crystal structure of the novel alpha-amylase amyc from thermotoga2 maritima
43	d1tuca_	Alignment	not modelled	95.9	11	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
44	d1utia_	Alignment	not modelled	95.9	14	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
45	d1sema_	Alignment	not modelled	95.8	10	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
46	c2djqA_	Alignment	not modelled	95.7	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**sh3 domain containing ring finger 2; **PDBTitle:** the solution structure of the first sh3 domain of mouse sh32 domain containing ring finger 2
47	d1gria2	Alignment	not modelled	95.7	17	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
48	d1ng2a2	Alignment	not modelled	95.7	7	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
49	d1oeba_	Alignment	not modelled	95.7	16	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
50	d1ug1a_	Alignment	not modelled	95.7	19	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
51	d1wfwa_	Alignment	not modelled	95.6	13	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
52	c2df6A_	Alignment	not modelled	95.6	10	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**rho guanine nucleotide exchange factor 7; **PDBTitle:** crystal structure of the sh3 domain of betapix in complex2 with a high affinity peptide from pak2
53	c2dbkA_	Alignment	not modelled	95.6	16	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**crk-like protein; **PDBTitle:** solution structures of the sh3 domain of human crk-like2

						protein
54	d1ov3a2	Alignment	not modelled	95.6	30	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
55	c1x2pA_	Alignment	not modelled	95.6	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein arginine n-methyltransferase 2; **PDBTitle:** solution structure of the sh3 domain of the protein2 arginine n-methyltransferase 2
56	c2kbtA_	Alignment	not modelled	95.6	12	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**chimera of proto-oncogene vav, linker, **PDBTitle:** attachment of an nmr-invisible solubility enhancement tag2 (inset) using a sortase-mediated protein ligation method
57	c1r77A_	Alignment	not modelled	95.6	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cell wall targeting domain of glycylglycine **PDBTitle:** crystal structure of the cell wall targeting domain of2 peptidylglycan hydrolase ale-1
58	c1wyxA_	Alignment	not modelled	95.6	16	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**crk-associated substrate; **PDBTitle:** the crystal structure of the p130cas sh3 domain at 1.1 a2 resolution
59	c2dl3A_	Alignment	not modelled	95.5	13	**PDB header:**cell adhesion, signaling protein **Chain:** A: **PDB Molecule:**sorbin and sh3 domain-containing protein 1; **PDBTitle:** solution structure of the first sh3 domain of human sorbin2 and sh3 domain-containing protein 1
60	c2drmB_	Alignment	not modelled	95.5	12	**PDB header:**contractile protein **Chain:** B: **PDB Molecule:**acanthamoeba myosin ib; **PDBTitle:** acanthamoeba myosin i sh3 domain bound to acan125
61	d1udla_	Alignment	not modelled	95.4	12	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
62	d1uhfa_	Alignment	not modelled	95.3	14	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
63	d1uj0a_	Alignment	not modelled	95.3	11	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
64	c2j6kE_	Alignment	not modelled	95.3	11	**PDB header:**protein binding **Chain:** E: **PDB Molecule:**cd2-associated protein; **PDBTitle:** n-terminal sh3 domain of cms (cd2ap human homolog)
65	c2csqA_	Alignment	not modelled	95.3	10	**PDB header:**endocytosis/exocytosis **Chain:** A: **PDB Molecule:**rim binding protein 2; **PDBTitle:** solution structure of the second sh3 domain of human rim-2 binding protein 2
66	d1nega_	Alignment	not modelled	95.3	9	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
67	c1negA_	Alignment	not modelled	95.3	9	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**spectrin alpha chain, brain; **PDBTitle:** crystal structure analysis of n-and c-terminal labeled sh3-2 domain of alpha-chicken spectrin
68	d1oota_	Alignment	not modelled	95.3	15	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
69	d1uuea_	Alignment	not modelled	95.2	14	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
70	c2dilA_	Alignment	not modelled	95.2	21	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**proline-serine-threonine phosphatase-interacting **PDBTitle:** solution structure of the sh3 domain of the human proline-2 serine-threonine phosphatase-interacting protein 1
71	d1gcqa_	Alignment	not modelled	95.2	18	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
72	d1pwta_	Alignment	not modelled	95.2	12	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
73	c2yunA_	Alignment	not modelled	95.2	11	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**nostrin; **PDBTitle:** solution structure of the sh3 domain of human nostrin
74	c1zx6A_	Alignment	not modelled	95.2	24	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**ypr154wp; **PDBTitle:** high-resolution crystal structure of yeast pin3 sh3 domain
75	d1uffa_	Alignment	not modelled	95.1	12	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
76	d1u06a1	Alignment	not modelled	95.1	12	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
77	c2dl4A_	Alignment	not modelled	95.0	17	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**protein stac; **PDBTitle:** solution structure of the first sh3 domain of stac protein
78	d1gl5a_	Alignment	not modelled	95.0	9	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
79	c2d1xD_	Alignment	not modelled	95.0	11	**PDB header:**cell invasion **Chain:** D: **PDB Molecule:**cortactin isoform a; **PDBTitle:** the crystal structure of the cortactin-sh3 domain and amap1-2 peptide complex

80	c1w70A_	Alignment	not modelled	95.0	5	**PDB header:**sh3 domain **Chain:** A: **PDB Molecule:**neutrophil cytosol factor 4; **PDBTitle:** sh3 domain of p40phox complexed with c-terminal polyproline2 region of p47phox
81	c2dnuA_	Alignment	not modelled	95.0	9	**PDB header:**structural genomics, structural protein **Chain:** A: **PDB Molecule:**sh3 multiple domains 1; **PDBTitle:** solution structure of rsgi ruh-061, a sh3 domain from human
82	c2krnA_	Alignment	not modelled	94.9	8	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**cd2-associated protein; **PDBTitle:** high resolution structure of the second sh3 domain of cd2ap
83	c1zlmA_	Alignment	not modelled	94.9	11	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**osteoclast stimulating factor 1; **PDBTitle:** crystal structure of the sh3 domain of human osteoclast2 stimulating factor
84	c1wi7A_	Alignment	not modelled	94.9	11	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**sh3-domain kinase binding protein 1; **PDBTitle:** solution structure of the sh3 domain of sh3-domain kinase2 binding protein 1
85	d1gbra_	Alignment	not modelled	94.8	17	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
86	d1k4us_	Alignment	not modelled	94.8	15	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
87	c2k6dA_	Alignment	not modelled	94.8	8	**PDB header:**sh3 domain/ubiquitin **Chain:** A: **PDB Molecule:**sh3 domain-containing kinase-binding protein 1; **PDBTitle:** cin85 sh3-c domain in complex with ubiquitin
88	c1x2qA_	Alignment	not modelled	94.8	13	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**signal transducing adapter molecule 2; **PDBTitle:** solution structure of the sh3 domain of the signal2 transducing adaptor molecule 2
89	c2epdA_	Alignment	not modelled	94.8	19	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**rho gtpase-activating protein 4; **PDBTitle:** solution structure of sh3 domain in rho-gtpase-activating2 protein 4
90	c2xmfA_	Alignment	not modelled	94.8	11	**PDB header:**motor protein **Chain:** A: **PDB Molecule:**myosin 1e sh3; **PDBTitle:** myosin 1e sh3
91	d1wlpb2	Alignment	not modelled	94.8	16	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
92	c2ebpA_	Alignment	not modelled	94.8	9	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**sam and sh3 domain-containing protein 1; **PDBTitle:** solution structure of the sh3 domain from human sam and sh32 domain containing protein 1
93	c2jxbA_	Alignment	not modelled	94.7	13	**PDB header:**signaling protein complex **Chain:** A: **PDB Molecule:**t-cell surface glycoprotein cd3 epsilon chain, **PDBTitle:** structure of cd3epsilon-nck2 first sh3 domain complex
94	c2dl8A_	Alignment	not modelled	94.7	7	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**slit-robo rho gtpase-activating protein 2; **PDBTitle:** solution structure of the sh3 domain of human slit-robo rho2 gtpase-activating protein 2
95	c2fg0B_	Alignment	not modelled	94.7	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cog0791: cell wall-associated hydrolases (invasion- **PDBTitle:** crystal structure of a putative gamma-d-glutamyl-l-diamino acid2 endopeptidase (npun_r0659) from nostoc punctiforme pcc 73102 at 1.793 a resolution
96	c2azsA_	Alignment	not modelled	94.7	18	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**sh2-sh3 adapter protein drk; **PDBTitle:** nmr structure of the n-terminal sh3 domain of drk2 (calculated without noe restraints)
97	c2ysqA_	Alignment	not modelled	94.6	12	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**rho guanine nucleotide exchange factor 9; **PDBTitle:** solution structure of the sh3 domain from rho guanine2 nucleotide exchange factor 9
98	c2dx1A_	Alignment	not modelled	94.6	16	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**rho guanine nucleotide exchange factor 4; **PDBTitle:** crystal structure of rhogef protein asef
99	c2a28D_	Alignment	not modelled	94.6	3	**PDB header:**signaling protein **Chain:** D: **PDB Molecule:**bzz1 protein; **PDBTitle:** atomic-resolution crystal structure of the second sh32 domain of yeast bzz1 determined from a pseudomerohedrally3 twinned crystal
100	c2dlpA_	Alignment	not modelled	94.6	16	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**kiaa1783 protein; **PDBTitle:** solution structure of the sh3 domain of human kiaa17832 protein
101	c1z9qA_	Alignment	not modelled	94.5	13	**PDB header:**oxidoreductase activator **Chain:** A: **PDB Molecule:**neutrophil cytosol factor 4; **PDBTitle:** solution structure of sh3 domain of p40phox
102	d1opka1	Alignment	not modelled	94.5	11	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
103	c2eyxA_	Alignment	not modelled	94.5	10	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**v-crk sarcoma virus ct10 oncogene homolog **PDBTitle:** c-terminal sh3 domain of ct10-regulated kinase
104	c2cubA_	Alignment	not modelled	94.5	6	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**cytoplasmic protein nck1; **PDBTitle:** solution structure of the sh3 domain of the human2 cytoplasmic protein nck1

105	c1x69A_	Alignment	not modelled	94.4	12	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**cortactin isoform a; **PDBTitle:** solution structures of the sh3 domain of human src2 substrate cortactin
106	d1ujya_	Alignment	not modelled	94.4	13	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
107	d1e6ga_	Alignment	not modelled	94.3	16	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
108	c2ed1A_	Alignment	not modelled	94.3	12	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**130 kda phosphatidylinositol 4,5-biphosphate- **PDBTitle:** solution structure of the sh3 domain of 130 kda2 phosphatidylinositol 4,5-biphosphate-dependent arf1 gtpase-3 activating protein
109	c2egaA_	Alignment	not modelled	94.3	14	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**sh3 and px domain-containing protein 2a; **PDBTitle:** solution structure of the first sh3 domain from human2 kiaa0418 protein
110	c2dybA_	Alignment	not modelled	94.3	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**neutrophil cytosol factor 4; **PDBTitle:** the crystal structure of human p40(phox)
111	d1e6ha_	Alignment	not modelled	94.3	16	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
112	c2csiA_	Alignment	not modelled	94.2	26	**PDB header:**endocytosis/exocytosis **Chain:** A: **PDB Molecule:**rim binding protein 2; **PDBTitle:** solution structure of the third sh3 domain of human rim-2 binding protein 2
113	d1ov3a1	Alignment	not modelled	94.2	16	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
114	c2bz8B_	Alignment	not modelled	94.2	13	**PDB header:**sh3 domain **Chain:** B: **PDB Molecule:**sh3-domain kinase binding protein 1; **PDBTitle:** n-terminal sh3 domain of cin85 bound to cbl-b peptide
115	c2js0A_	Alignment	not modelled	94.2	10	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**cytoplasmic protein nck1; **PDBTitle:** solution structure of second sh3 domain of adaptor nck
116	d2fo0a1	Alignment	not modelled	94.1	11	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
117	d1j3ta_	Alignment	not modelled	93.9	17	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
118	c1x43A_	Alignment	not modelled	93.9	14	**PDB header:**endocytosis/exocytosis **Chain:** A: **PDB Molecule:**sh3 domain grb2-like protein b1; **PDBTitle:** solution structure of the sh3 domain of endophilin b12 (sh3g1b1)
119	c2l0aA_	Alignment	not modelled	93.9	8	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**signal transducing adapter molecule 1; **PDBTitle:** solution nmr structure of signal transducing adapter molecule 1 stam-12 from homo sapiens, northeast structural genomics consortium target3 hr4479e
120	d1lcka1	Alignment	not modelled	93.9	11	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain